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ESULT 1
METK_NEIMB
ID   METK_NEIMB              Reviewed;         389 AA.
AC   Q9JY09;
DT   02-AUG-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2000, sequence version 1.
DT   04-NOV-2008, entry version 50.
DE   RecName: Full=S-adenosylmethionine synthetase;
DE            EC=2.5.1.6;
DE   AltName: Full=Methionine adenosyltransferase;
DE   AltName: Full=AdoMet synthetase;
DE   AltName: Full=MAT;
GN   Name=metK; OrderedLocusNames=NMB1799;
OS   Neisseria meningitidis serogroup B.
CC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
CC   Neisseriaceae; Neisseria.
OX   NCBI_TaxID=491;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MC58 / Serogroup B;
RX   MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA   Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA   Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA   Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA   Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA   Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA   Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA   Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
RA   Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA   Venter J.C.;
RT   "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT   MC58.";
RL   Science 287:1809-1815(2000).
CC   -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC       methionine and ATP. The overall synthetic reaction is composed of
CC       two sequential steps, AdoMet formation and the subsequent
CC       tripolyphosphate hydrolysis which occurs prior to release of
CC       AdoMet from the enzyme (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC       diphosphate + S-adenosyl-L-methionine.
CC   -!- COFACTOR: Binds 2 divalent ions per subunit. Magnesium or cobalt
CC       (By similarity).
CC   -!- COFACTOR: Binds 1 potassium ion per subunit (By similarity).
CC   -!- PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methionine
CC       biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.
CC   -!- SUBUNIT: Homotetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasm.
CC   -!- SIMILARITY: Belongs to the AdoMet synthetase family.
CC   ----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; AE002098; AAF42136.1; -; Genomic_DNA.
DR   PIR; D81042; D81042.
DR   RefSeq; NP_274796.1; -.
DR   HSSP; P04384; 1MXB.
DR   GeneID; 903300; -.
DR   GenomeReviews; AE002098_GR; NMB1799.
DR   KEGG; nme:NMB1799; -.
DR   NMPDR; fig|122586.1.peg.1730; -.
DR   TIGR; NMB1799; -.
DR   HOGENOM; Q9JY09; -.
DR   BioCyc; NMEN122586:NMB_1799-MON; -.
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DR   GO; GO:0005737; C:cytoplasm; IEA:HAMAP.
DR   GO; GO:0005524; F:ATP binding; IEA:HAMAP.
DR   GO; GO:0050897; F:cobalt ion binding; IEA:UniProtKB-KW.
DR   GO; GO:0000287; F:magnesium ion binding; IEA:HAMAP.
DR   GO; GO:0004478; F:methionine adenosyltransferase activity; IEA:HAMAP.
DR   GO; GO:0030955; F:potassium ion binding; IEA:UniProtKB-KW.
DR   GO; GO:0006730; P:one-carbon compound metabolic process; IEA:HAMAP.
DR   HAMAP; MF_00086; -; 1.
DR   InterPro; IPR002133; S-AdoMet_synthetase.
DR   PANTHER; PTHR11964; S-AdoMet_synt; 1.
DR   Pfam; PF02773; S-AdoMet_synt_C; 1.
DR   Pfam; PF02772; S-AdoMet_synt_M; 1.
DR   Pfam; PF00438; S-AdoMet_synt_N; 1.
DR   PIRSF; PIRSF000497; MAT; 1.
DR   TIGRFAMs; TIGR01034; metK; 1.
DR   PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR   PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
PE   3: Inferred from homology;
KW   ATP-binding; Cobalt; Complete proteome; Cytoplasm; Magnesium;
KW   Metal-binding; Nucleotide-binding; One-carbon metabolism; Potassium;
KW   Transferase.
FT   CHAIN           1       389       S-adenosylmethionine synthetase.
FT                                     /FTId=PRO_0000174560.
FT   NP_BIND       264     271         ATP (Potential).
FT   METAL          17      17         Magnesium (By similarity).
FT   METAL          43      43         Potassium (By similarity).
FT   METAL         268     268         Potassium (By similarity).
FT   METAL         276     276         Magnesium (By similarity).
SQ   SEQUENCE   389 AA;  42099 MW;  18F4E98E56064FA7 CRC64;

  Query Match             100.0%;  Score 2003;  DB 1;  Length 389;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-148;
  Matches  389;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSEYLFTSESVSEGHPDKVADQVSDAILDAILAQDPKARVAAETLVNTGLCVLAGEITTT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSEYLFTSESVSEGHPDKVADQVSDAILDAILAQDPKARVAAETLVNTGLCVLAGEITTT 60

Qy         61 AQVDYIKVARETIKRIGYNSSELGFDANGCAVGVYYDQQSPDIAQGVNEGEGIDLNQGAG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AQVDYIKVARETIKRIGYNSSELGFDANGCAVGVYYDQQSPDIAQGVNEGEGIDLNQGAG 120

Qy        121 DQGLMFGYACDETPTLMPFAIYYSHRLMQRQSELRKDGRLPWLRPDAKAQLTVVYDSETG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DQGLMFGYACDETPTLMPFAIYYSHRLMQRQSELRKDGRLPWLRPDAKAQLTVVYDSETG 180

Qy        181 KVKRIDTVVLSTQHDPSIAYEELKNAVIEHIIKPVLPSELLTDETKYLINPTGRFVIGGP 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KVKRIDTVVLSTQHDPSIAYEELKNAVIEHIIKPVLPSELLTDETKYLINPTGRFVIGGP 240

Qy        241 QGDCGLTGRKIIVDTYGGAAPHGGGAFSGKDPSKVDRSAAYACRYVAKNIVAAGLATQCQ 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QGDCGLTGRKIIVDTYGGAAPHGGGAFSGKDPSKVDRSAAYACRYVAKNIVAAGLATQCQ 300

Qy        301 IQVSYAIGVAEPTSISIDTFGTGKISEEKLIALVREHFDLRPKGIVQMLDLLRPIYSKSA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IQVSYAIGVAEPTSISIDTFGTGKISEEKLIALVREHFDLRPKGIVQMLDLLRPIYSKSA 360

Qy        361 AYGHFGREEPEFTWERTDKAAALRAAAGL 389
              |||||||||||||||||||||||||||||
Db        361 AYGHFGREEPEFTWERTDKAAALRAAAGL 389
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